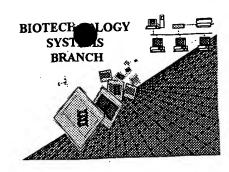
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/938,842

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

OIPE

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DATE: 09/13/2001
                        RAW SEQUENCE LISTING
                        PATENT APPLICATION: US/09/938,842
                                                                TIME: 16:32:16
                        Input Set : N:\paola\09938842.txt
                        Output Set: N:\CRF3\09132001\I938842.raw
                                                                                 Does Not Comply
                                                                             Corrected Diskette Needed
         1 <110> APPLICANT: Harper, Jeff
                 Kreps, Joel
                 Wang, Xun
         3
                 Zhu, Tong
         6 <120> TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS
   CONTAINING SAME, AND I MINING WAY
               METHODS OF USE
         9 <130> FILE REFERENCE: SCRIP1300-3
  > 11 <140 > CURRENT APPLICATION NUMBER: US/09/938,842 
> 11 <141 > CURRENT FILING DATE: 2001-08-24
                                                              un Alis' date format
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   w--> 12 <151> PRIOR FILING DATE: (2000-8-24) 2000-08-29
        14 <150> PRIOR APPLICATION NUMBER: US 60/264,647
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        17 <150> PRIOR APPLICATION NUMBER: US 60/300,111
   W--> 18 <151> PRIOR FILING DATE: (2001-6-22) 2001-06-22
       20 <160> NUMBER OF SEQ ID NOS: 5379
   ERRORED SEQUENCES
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        15510 <211> LENGTH: 421
        15511 <212> TYPE: DNA
   15512 <213> ORGANISM: Arabidopsis thaliana
        15514 <220> FEATURE:
αγ<sup>μ</sup> 15516 <222> LOCATION: (3)..(3)

2 γ γ α 15517 <223> ΟΤΗΡΡ ΤΗΡΟΙΙΑ
       15515 <221> NAME/KEY: N_region
        15517 < 223 > OTHER INFORMATION: n = any nucleotide
                                               -) slashes are im
             <400> SEQUENCE: 304
              //hcqfj tgg ctttcgagcg gccgcccggg caggtaaccc acctttatta ccattcaggt
                                                                                     60
   E--> 15522 ttcagaacct aggtgagatg atgactettg gaagatatea ttetgetata tececaagtt
                                                                                    120
   E--> 15524 tcattgaagg gcttaccctt gaagtttcaa ttggtcacgc agcgagaaaa ctggcgtatt
                                                                                    180
   E--> 15526 tgattagact tccaactgat gaaccccggt ttaaggtcgg aatcagttgg tttgctaaat
                                                                                    240
                                                                                    300
   E--> 15528 ctgctgttga ttcaattgct ttacttcaga gcaatctaac caaggttttg tctggttctt
   E--> 15530 gatctccgtt tgttttgctt tggagattaa ttcgcttccg tatgaaagac aaatggggag
                                                                                    360
   420
   E--> 15534 a
                                                                                    421
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        89511 <211> LENGTH: 467
        89512 <212> TYPE: DNA
        89513 <213> ORGANISM: Arabidopsis thaliana
        89515 <220> FEATURE:
        89516 <221> NAME/KEY: N_region
        89517 <222> LOCATION: (3)..(3)
        89518 <223> OTHER INFORMATION: n = any nucleotide
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(/ncgi) att gggtttacag tttactagac cagatgtggt ggggtttggg tacaaaaggg

sameen

E--> 89521

89520 <400> SEQUENCE: 1784

RAW SEQUENCE LISTING

DATE: 09/13/2001

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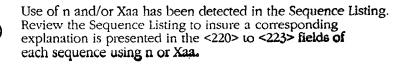
PATENT APPLICATION: US/09/938,842

TIME: 16:32:24

Input Set : N:\paola\09938842.txt

Output Set: N:\CRF3\09132001\1938842.raw

		h 0.
E>	89523 ccagactggt tttcgaagtt gcaaaatgga aaaactgatc agcaggcggg ataggacggg	120
E>	89525 gctggtccac aggctacagc ctacaggttg atcatacata cctaaaacct ataatcagtt	180
E>	89527 taggcagata tagtagcctt acaagttaga actatctcaa ttcataagtc ccaagtccct	240
E>	89529 aagccctcct ttgccatggc tctttgtgaa actagcactt taagataatc gcattttctc	300
E>	89531 tcatctcctt gggcctctca caaactaaat tttgtgggca acttcaatct tggtttctag	360
E>	89533 tatatgtgca aagatattaa aatcagtata aaattagtta gtgttagtat ttggagttta	420
E>	89535 taaatttaaa aatatctact acttcaatca aaagtcgacg cggccgc	467
	123106 <210> SEQ ID NO: 2469	
	123107 <211> LENGTH: (245)	*
	123108 <212> TYPE: DNA	
	123109 <213> ORGANISM: Arabidopsis thaliana	
	123111 <220> FEATURE:	
	123112 <221> NAME/KEY: N_region /	
	123112 <221> NAME/REI: N_legion 123113 <222> LOCATION: (3)(3) 123114 <223> OTHER INFORMATION: n = any nucleotide 123116 <400> SEQUENCE: 2469	
	123114 <223> OTHER INFORMATION: n = any nucleotide	_
	123116 <400>, SEQUENCE: 2469	0009
E>	123117 //ncgi/tcg agcggccgcc cgggcaggta ccaaaccgga aaatacagtc tcatactttt	(69/3/
E>	123119 addttttct gtttcagagt aagagatgac tgctcttcct cctcttgttg aggaaaccat	120 /
E>	123121 cttctccact taatttccat aatttccttg ctttgtagga gttacgactc cacttttttg	180 🗸
E>	123123 cttcttgtaa tgtttctcta tttaaaaaaaa accaaaaaaa aaaaaaaa	240
E>	123125 aaaaa	245



VERIFICATION SUMMARY PATENT APPLICATION: US/09/938,842

DATE: 09/13/2001 TIME: 16:32:49

Input Set : N:\paola\09938842.txt

Output Set: N:\CRF3\09132001\I938842.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD L:15520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304 L:15520 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:304 L:15520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 M:254 Repeated in SeqNo=304 L:15534 M:252 E: No. of Seq. differs, <211>LENGTH:Input:421 Found:419 SEQ:304 L:89521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1784 L:89521 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:1784 L:89521 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 M:254 Repeated in SegNo=1784 L:89535 M:252 E: No. of Seq. differs, <211>LENGTH:Input:467 Found:465 SEQ:1784 L:123117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2469 L:123117 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:58 SEQ:2469 L:123117 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 M:254 Repeated in SeqNo=2469 L:123125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:245 Found:243 SEQ:2469

L:179888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3467 L:205509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3913